

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus.p2n model

Run on: May 30, 2003, 04:18:46 ; Search time 3433 Seconds  
(without alignments) 3433.334 Million cell updates/sec

Title: US-09-934-900-2  
Perfect score: 2150  
Sequence: 1 MLSIFKEFEVYNNRHVIKTM.....KMKKHGVKFSWIFNKELL 405

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2054640 segs, 14551402878 residues  
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ p2n.model -DEV=xlh  
-O=/cgn2.1/USFPO/us09934900/runat\_23052003.160451.15193/app.query.fasta.1.583  
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-ONITS=bits -START=1 -END=1 -MATRIX=blsum62 -TRANS=human40.cdi -LIST=45  
-DOCALLIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09934900.ecgn.1.12496.8runat.23052003.160451.15193 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGOQUERY -NEG.SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:\*  
1: gb.ba:\*  
2: gb.htg:\*  
3: gb.in:\*  
4: gb.om:\*  
5: gb.ov:\*  
6: gb.pat:\*  
7: gb.ph:\*  
8: gb.pl:\*  
9: gb.pr:\*  
10: gb.ro:\*  
11: gb.sts:\*  
12: gb.sy:\*  
13: gb.un:\*  
14: gb.vl:\*  
15: em.ba:\*  
16: em.fun:\*  
17: em.hum:\*  
18: em.in:\*  
19: em.mu:\*  
20: em.om:\*  
21: em.or:\*  
22: em.ov:\*  
23: em.pat:\*  
24: em.ph:\*  
25: em.pl:\*  
26: em.ro:\*  
27: em.sts:\*  
28: em.un:\*

29: em.vl:\*  
30: em.htg.hum:\*  
31: em.htg.in:\*  
32: em.htg.other:\*  
33: em.htg.mus:\*  
34: em.htg.pln:\*  
35: em.htg.rod:\*  
36: em.htg.mam:\*  
37: em.htg.vrt:\*  
38: em.sy:\*  
39: em.htgo.hum:\*  
40: em.htgo.mus:\*  
41: em.htgo.other:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2150	100.0	1560	6	AX392312 Sequence
2	1661	77.3	1717	6	AX367139 Sequence
3	1646	76.6	1470	8	AF139377 Lupinus 1
4	1466	68.2	1395	8	AY085086 Arabidops
5	1394	64.8	1284	8	AS060377 Arabidops
6	1338.5	62.3	1415	6	AX392322 Sequence
7	1337	62.2	1337	8	TAU07597 Thunbergia
8	1322.5	61.5	1318	6	AX392326 Sequence
9	1317	61.3	1576	8	SMNSCPD
10	1313	61.1	1443	8	TAU07605 Thunbergia
11	1306	60.7	1507	8	POTSACPD
12	1301	60.5	1651	8	AY087294 Arabidops
13	1300	60.5	1243	6	I13990 Sequence 1
14	1299	60.4	1643	8	RCCSACPD
15	1298	60.4	1279	8	AY128883 Arabidops
16	1298	60.4	1583	8	AY099784 Arabidops
17	1296.5	60.3	1407	8	CUSACPD
18	1295.5	60.3	1768	8	SCSACPD
19	1295	60.2	1662	6	RCSSTA
20	1295	60.2	1668	6	I90191 Sequence 15
21	1292	60.1	1319	8	TAU07552 Thunbergia
22	1291	60.0	1200	8	AF315600 Bassia sc
23	1288	59.9	131692	8	AC006423 Arabidops
24	1283	59.7	1533	6	I16556 Sequence 32
25	1283	59.7	1533	6	I19664 Sequence 32
26	1283	59.7	1533	6	I90189 Sequence 12
27	1283	59.7	1533	8	CAHSACPD
28	1279	59.5	1610	8	SONACPD
29	1278.5	59.5	1235	8	HAU91339 Helianthus
30	1278	59.4	1580	8	SSMSACPD
31	1276.5	59.4	1623	8	SOVSACPD
32	1271.5	59.1	168033	2	AP003405 Oryza sat
33	1271.5	59.1	200183	8	AP003227 Oryza sat
34	1270	59.1	1493	8	OEUS8141 Olea europ
35	1268.5	59.0	1426	8	HAU91340 Helianthus
36	1266	58.9	1517	8	AF116861 Persia am
37	1266	58.9	1524	6	A74273 Sequence 3
38	1266	58.9	1524	6	BNSACPD
39	1265.5	58.9	1715	8	EGU68756 Arabidops
40	1263	58.7	1495	6	I90194 Sequence 19
41	1263	58.7	1495	8	BRNACP
42	1263	58.7	1516	8	BNACPD
43	1260	58.6	1548	8	AF172728 Arabidops
44	1259	58.6	1567	8	AY088096 Arabidops
45	1258.5	58.5	1206	8	AF395441 Arabidops

RESULT 1

## ALIGNMENTS

AX392312 1560 bp DNA linear PAT 23-MAR-2002  
 LOCUS AX392312  
 DEFINITION Sequence 1 from Patent WO0216565.  
 ACCESSION AX392312  
 VERSION AX392312.1 GI:19700680  
 KEYWORDS  
 SOURCE soybean.  
 ORGANISM Glycine max  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eustosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
 Glycine.  
 REFERENCE 1  
 AUTHORS Booth, J.R., Cahoon, R.E., Hitz, W.D., Kinney, A.J. and Yadav, N.S.  
 TITLE Nucleotide sequences of a new class of diverged delta-9  
 steroyl-acp desaturase genes  
 JOURNAL Patent: WO 0216565-A 1 28-FEB-2002;  
 E. I. du Pont de Nemours and Company (US)  
 FEATURES  
 source Location/Qualifiers  
 1. 1560  
 /organism="Glycine max"  
 /db\_xref="taxon:3847"  
 BASE COUNT 402 a 360 c 443 g 355 t  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 7.59e-167 Length: 1560  
 Score: 2150.00 Matches: 405  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: Gaps: 0  
 US-09-934-900-2 (1-405) x AX392312 (1-1560)

DB 647 GAGGAAACAGACACGGGAGTCTCAGAACTATTGTTATCTCTCGGAGGCTTAC 706  
 QY 201 MetAlaValAlaGluPheThrValHisTyrLeuIleSerAlaGlyMetAspProGlyThr 220  
 DB 707 ATGGCTAAGTGTGAAAGACCGTACATTACCTATTTCAGCTGGCATGGACCTGGGAGA 766  
 QY 221 AspAsnAsnProTyrLeuGlyPheValTyrThrSerPheGlnGluArgAlaThrPheVal 240  
 DB 767 GACAACACCCATATTGTTGGGTTTGTGTACAGTCATTCCAGAGGACGACCAATTTGTG 826  
 QY 241 AlaHisGlyAsnThrAlaArgLeuAlaValGlyGlyGlyAspProValLeuAlaArgLeu 260  
 DB 827 GCGCAGGGAGACACGGCTCGCTCGGAGAGGGGGGGGATTCACATGCTGGCGGCTTA 886  
 QY 261 CysGlyThrIleAlaAlaAspGluValArgHisGlnAlaValTyrSerArgIleValGlu 280  
 DB 887 TCGGGACCATCGACCGACGACGAGAGCGGACAGAACCGGTACTCAAGAACTCGGGAG 946  
 QY 281 LysLeuLeuGluValAspProThrGlyAlaMetValAlaIleGlyAsnMetMetGlyLys 300  
 DB 947 AAGCTTCTGAAAGTGGACCCACCGGGGCAATGTGTCATAGGAAATGATGGAGAAG 1006  
 QY 301 LysIleThrMetProAlaHisLeuMetTyrAspGlyAspAspProArgLeuPheGlnHis 320  
 DB 1007 AAGATTCAGATGCGGCGACCTTATGTACGATGGAGATGCCACAGCTATTCCAGAC 1066  
 QY 321 TyrSerAlaValAlaGlnArgGlyIleGlyValTyrThrAlaAsnAspTyrAlaAspIleLeu 340  
 DB 1067 TACTCGCGTGTGGCGGACGACGACGATGACGCTACACCGCACAGACTACGACATCTTG 1126  
 QY 341 GluPheLeuValGluArgTyrPheArgLeuGluLysLeuGlyGlyLeuMetAlaGluLys 360  
 DB 1127 GAGTTTCTGTTGAACGGTGGAGATGGAGAAAGCTTGAAGATTTGATGCTGAGGGGAAG 1186  
 QY 361 ArgAlaGlnAspPheValGlyGlyLeuAlaProArgIleArgArgLeuGlnGluArgAla 380  
 DB 1187 CCGGCGCAGAGTTTCTGTGTGGGTGGCGGCGGAGATTGAGGTTGCAAGACCGGCT 1246  
 QY 381 AspGluArgAlaArgLysMetLysLysHisGlyValLysPheSerTyrIlePheAsn 400  
 DB 1247 GATGACGACGCGCGTAAAGTGAAGAACATCATGGCGTTAATGCTGATTTTCAT 1306  
 QY 401 LysGluLeuLeuLeu 405  
 DB 1307 AAAAATTCCTTTTG 1321  
 RESULT 2  
 LOCUS AX367139 1717 bp DNA linear PAT 16-FEB-2002  
 DEFINITION Sequence 24 from Patent WO020904.  
 ACCESSION AX367139  
 VERSION AX367139.1 GI:1885340  
 KEYWORDS  
 SOURCE synthetic construct.  
 ORGANISM synthetic construct  
 REFERENCE 1  
 AUTHORS Glassman, K.F., Gordon-Kamm, W.J., Kinney, A.J., Lowe, K., Stecca, K.L.  
 and Nichols, S.E.  
 TITLE Recombinant constructs and their use in reducing gene expression  
 JOURNAL Patent: WO 020904-A 24 03-JAN-2002;  
 E. I. du Pont de Nemours and Company (US) ; PIONEER HI-BRED  
 INTERNATIONAL, INC. (US)  
 FEATURES  
 source Location/Qualifiers  
 1. 1717  
 /organism="synthetic construct"  
 /db\_xref="taxon:32630"  
 /note="ELVISLIVES complementary region of pBS68"  
 BASE COUNT 399 a 430 c 478 g 410 t  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 9.29e-127 Length: 1717

Score:	1661.00	Matches:	331
Percent Similarity:	95.95%	Conservative:	1
Best Local Similarity:	95.66%	Mismatches:	10
Query Match:	77.26%	Indels:	6
DB:	6	Gaps:	1

US-09-934-900-2 (1-405) \* AX367139 (1-1717)

OY	64	ArgValAlaHisSerMetProGluLysArgLysGluIlePheLysSerLeuGluGlyTrp	83
Db	641	AGATTAAAGCCGCCCATCTCCTCCGAAAAGAAATTTTCAAGTCCTTGAGGGAGTGG	700
OY	84	AlaSerGluTrpValLeuProLeuLeuLysProValGluIncYstrPGlnProGlnAsn	103
Db	701	GCTCGGAGTGGGTCTACCCGCTGTAAGCCCGTAGAGCAATGCTGGCACCAAMAAC	760
OY	104	PheLeuProAspProSerLeuProHisGluLubheserHisGlnValLysGluLeuArg	123
Db	761	TTCCTCCCTGCACCCTCCCTCCCATGMAAGAATTCACCCACTACAGTGAAGACGCTTCGC	820
OY	124	GluArgThrLysGluLeuProAspGluTrpPheValValLeuValAlaGlyAspMetValThr	143
Db	821	GAAGCGACAATAAGAGTAACTCGATGAGTACTTTTGCTGGCTGGGTGGATATGTCAC	880
OY	144	GluAspAlaLeuProThrTyrgLInthrMetIleasnAsnLeuAspGlyValLysAspAsp	163
Db	881	GAGAGACGGCTCCCATCTTACCAACCATGATCAACAACCTTGATGAGTGAAGATGAC	940
OY	164	SerGlyIthrSerProSerProTrpAlaValTrpThrArgAlaTrpThrAlaGluGlnAsn	183
Db	941	AGCGGACAGACCCGAGACCGGTGGCGCTGTGGACCCGCGCTGGACCGCGAGGAAAAAC	1000
OY	184	ArgHisGlyAspLeuLeuArgThrTyrgLeuTyrgLeuSerGlyArgValAspMetAlaLys	203
Db	1001	AGACACGGGGATCTGCTCAGAACCTATTGTATCTCTCTGGGAGGGTTGACATGGCTAAG	1066
OY	204	ValGluLysThrValHisTrpLeuIleSeraIaGlyMetaSpProGlyTrpThrAspAsnAsn	223
Db	1061	GTCGAAAAAGACCGTACATTTACCTCATTTCCACTGGCATGGACCGCCGGAGACAAACAAC	1120
OY	224	ProTyrgLeuGlyPheValTyrgThrSerPheGlnGluArgAlaThrPheValAlaHisGly	243
Db	1121	CCATATTTGGGGTTGTGTACACGTCATTTCCAAGCGACAGAACATTTGTGGCGACGGG	1180
OY	244	AsnThrAlaArgLeuAlaLysGluGlyLysAspProValIleu---AlaArgLeuCysGlu	262
Db	1181	AACACGGCTGGGCTCTCGCAAGAGAGGCGGGGATCCAGTGTCTGGCGCGGCTTATGGCGG	1246
OY	262	YThrIleAlaAlaAspGluLysArgHisGluAsnAlaTyrgSerArgIleValGluLysIle	282
Db	1241	GACCATCGCACGGACGAGAGCGGACAGAACCGTAACTCAAGAATCGTGGAGAACT	1300
OY	282	ULeuGluValAspProThrArgLysIleMetValAlaIleLysAsnMetGluLysLysIle	302
Db	1301	TCTCGAAATGGACCCACCGGGGCAATGTGGCCATTAGGAACAATGAGAGAGAAACAAAT	1366
OY	302	eThrMetProAlaHisLeuMetTyrgAspGlyAspAspProArgLeuPheGluHisTyrgSe	322
Db	1361	CACGATGCCGGCGCACCTTATGTACGATGGGGATGACCCCAAGGCTATTGAGACACTACTC	1422
OY	322	IalaValAlaGlnArgIleGlyValTyrgThrAlaAsnAspTyrgAlaAspIleLeuGluPh	342
Db	1421	CGGTGTGGCGACGACATAGGCGTGTACCCGCAACGACATACGACAGACATCTTGA--TT	1479
OY	342	eLeuValGluArgTrpArgLeuGluLysLeuGluGluLysMetAlaGluGlyLysArgAl	362
Db	1480	TCTCGCTTTGA-CGGTGAACATTTGGAAACCTTGAAAGATTTGATCGCTGAGGGGAAACGGCGC	1538
OY	362	a-GlnAspPhe-ValCysGlyLeuAlaProArgIleArgArgLeuGluGluArgAlaAsp	381
Db	1539	CCCAGGATTCCTGCTGTGTGGGTGTGGCCCCCGAGAGATTTAGAGAGTTCCAAAGAACGCGCTGAT	1599
OY	382	GluArgAlaArgLysMetLysHisHisGlyValLysPheSerTrpIlePheAsnLys	401

Accession	Sequence	Position
Dd	1539 GAGGAGGCGCCTAAGATGAAAGAGCATCATCCCGTTAAGTCAGTTGATTTCAATAAA	1658
Qy	402 GluteuLeuLeu 405	
Dd	1659 GAATTGCTTTTG 1670	

RESULT 3  
AF139377

AF139377

LOCUS	AF139377	1470 bp	mRNA	linear	PLN 17-MAR-2000
DEFINITION	Lupinus luteus stearyl acyl carrier protein desaturase L1dd3A20				

ACCESSION	mRNA, complete cds.
AF139377	
AF139377.1	GI:4704823
VERSION	

KEYWORDS	AF133511.1	GI:4/04023
VERSION		
SOURCE		
	Lupinus luteus.	

ORGANISM  
Lupinus luteus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Genisteae;

Lupinus.  
1 (bases 1 to 1470)

**TITLE** Identification of new nodulin cDNAs from yellow lupine by differential display

JOURNAL  
REFERENCE  
2 (bases 1 to 1470)  
Plant Sci. 151 (1), 75-83 (2000)  
differential display

ANNOUNCED  
 2 (PAGES 1 TO 147)  
 AUTHORS  
 Swiderski, M. R., Zaborowska, Z. and Legocki, A. B.  
 TITLE  
 Direct Substitution

JOURNAL Submitted (30-MAR-1999) Biology, Indiana University, Jordan Hall 142, Bloomington 47405, USA

FEATURES	Location/Qualifiers
source	1. .1470

```

/organism="Lupinus luteus"
/cultivar="Ventus"
/ab_vrof="Favon, 1973"

```

```

CDS      .      /cd_xref="taxon:38/3"
          115..1269
          /codon_start=1

```

```

/cooem_start=1
/product="stearoyl acyl carrier protein desaturase
l1dd3A20"

```

```

/protein_id="AAD28287.1"
/db_xref="GI:4704824"

```

```
/translation="MOTQTCYSRIQILPLPARRTGHHKMLPPIAIAISATPSLSKSK  
KTHSMPEKIEIFKSLESMASQSVPLAKPVECSWQGFVFDSSLPGRGFTIQVKAL
```

RTORTAELPEEYFVLVGDMITEDALPTVQSMINNDGREDETGSSPSWALNTRAWTH  
EKRHGDDLRTLYLISGRVDMKTEKPYQLLIGSGMDPGTENNPYLGEVTSFOERAR  
EHWQWQDRLVGGDQDHTLPGQGGTLLGSGMDPGTENNPYLGEVTSFOERAR

FVSHGNTARLAKNEGDPYLARTCGTIADEKKEHNAHSRIVEKLLEDDPTGANVAIG  
EYMKQKITMPAHLMDYGEDPKLFEDHSAQAQRGVNLTADILLEFLIGRWREKVOQ  
YDEKZKAODEUCI ADPIRI OBRABDA PWRDPAWREGCENIZETI #

BASE COUNT 431 a 304 c 352 g 383 t  
ORIGIN LNDGGKKAQDVCGLAPRIIRLRQDERAEAKRKKKPHAVKFSWLNKELL"

Alignment Scores:

regimental colors:	
Pred. No.:	1.29e-125
Score:	1646.00
	Matches:
	1470
	311

Percent Similarity:	90.00%	Conservative:	40
Best Local Similarity:	79.74%	Mismatches:	33

Query Match:	76.56%	Indels:	6
DB:	8	Gaps:	5

US-09-934-900-2 (1-405) x AF139377 (1-1470)

18 Lys<sup>Thr</sup>Met<sup>Cln</sup>Ile<sup>Arg</sup>Thr<sup>Cys</sup>Ile<sup>Ser</sup>Ile<sup>Thr</sup>Thr<sup>Gln</sup>Ile<sup>Thr</sup>Leu<sup>Pro</sup>Gln<sup>Leu</sup>Pro 37

Db 109 AAAACATCGAGATTCAAACCTGCTACTATCAGAAATTCAAATTCCTCT---CTTCA 165

Oy 38 CysSerSerArgLysAlaIleHisHISArgHisLeuProProLeuAsnalaalValSer 57  
::: ||| ::|||::: |||::: |||::: |||

Db 166 TGGGCCAAGAAGACTGGCCGCCACAAA---ATGCTGCCACCCATA---GCAGCCATCTCC 219

58 Alalapro-----PhelysAlaArgLysAlaHisSerMetProGluIuLysLysGlu 75

DB 220 GCCACACCGCGCTGAAATCTCCTAAGACCCACTCATATGCCACACAGAAAAAGATAGAG 2/9

```

QY 76 11aPhelysSerLeuGluGlyTrpAlaSerGluTrpValLeuProLeuLeuLysProVal 95
Db 280 ATATCAAGTCACTTGAGAGCTGGGACATCAACATCGGTGCTTCACCTTGGAAGCCAGTG 339
QY 96 GluGlnCysTrpGlnProGlnAsnPhelProAspProSerLeuProHisGluGluPhe 115
Db 340 GAACAAATGCTGGACGCCAAGAATGCTCCCTGACCCCTTCCTGCGTTGGGGAATTC 399
QY 116 SerHisGlnValLysGluLeuArgGluArgGluThrLysGluLeuProAspGluTrpPheVal 135
Db 400 ACGGATCAGCTGAAGGCCCTCCGCTGACCGACGCGGAGAGCTGCCGGAGGAGTACTTCTG 459
QY 136 ValLeuValGlyAspMetValThrGluAspAlaLeuProThrTrpGlnThrMetLeuAsn 155
Db 460 GTATTGGTGGTGCATGATACAGAGAGATGCCGTGCCAAGTACAGACATGATCAAC 519
QY 156 AsnLeuAspGlyValLysAspAspSerGlyThrSerProSerProTrpAlaValTrpThr 175
Db 520 AATCTTGATGGGTGAAGGATGAGACTGGGTCAAGCCGACGCCATGGCTTTATGGACC 579
QY 176 ArgAlaTrpThrAlaGluGluAsnArgHisGlyAspLeuLeuArgThrTrpLeuTrpLeu 195
Db 580 CGGGCTTGACCTGCAGAGAGAAAGACATGAGATTTGCTTGAACCTTATTTGTATCTT 639
QY 196 SerGlyArgValAspMetAlaLysValGluLysThrValHisTrpLeuLeuSerAlaGly 215
Db 640 TCTGCTGCTGTTGATATGAGAGATGAGAGATGAGATGCTGATGATGATGATGATGCTG 699
QY 216 MetAspProGlyThrAspAsnAsnProTrpLeuGlyPheValTrpThrSerPheGlnGlu 235
Db 700 ATGAGCCCGGGGACAGAAACCAACCCATATTTGGGATTTGTATACAGCTATTTCCAGAG 759
QY 236 ArgAlaThrPheValAlaHisGlyAsnThrAlaArgLeuAlaLysGluGlyAspPro 255
Db 760 CGAGCCCATTTGCTGACATGGCAACACAGCTCGCTACCAAGAGGGTGGCGATCCA 819
QY 256 ValLeuAlaArgLeuGlyGlyThrThrLeaAlaAspGluLysArgHisGluAsnAlaTrp 275
Db 820 GTCTGCTGCTGATATGCGGACCATTTGCTGACAGACAGAAAGCCGACGAAATGCTAT 879
QY 276 SerArgGlyValGluLysLeuGluValAspProThrGlyAlaMetValAlaIleGly 295
Db 880 TCAGAGATGCTGCGAGAGCTTCTAGATTTGAGCCCAAGACGCAATGATGATTTGGA 939
QY 296 AsnMetMetGluLysLysIleThrMetProAlaHisLeuMetTrpAspGlyAspPro 315
Db 940 GACATGATGCGAGAAAGATCACATGCCACACTTGATGTACATGAGAGAACCTT 999
QY 316 ArgLeuPheGluHisTrpSerAlaValAlaGlnArgIleGlyValTrpThrAlaAsnAsp 335
Db 1000 AACTTGTGATCACTTCTGCGGCGGCGACGAAATGGGTTCACGCGCAATGAT 1059
QY 336 TyrAlaAspIleLeuGluPheLeuValGluArgTrpArgLeuGluLysLeuGluGluLeu 355
Db 1060 TATGCTGATATCTTGGAGTTTGTATCGAGCGGAGGATTTGGAAGAGTTCAAGATTTG 1119
QY 356 MetAlaGluGlyLysArgAlaGlnAspPheValCysGlyLeuAlaProArgIleArgArg 375
Db 1120 AAGGATGAGGGAAGAAAGACAGATTTGCTGTGTGGTGGCAGCGAGATCAGAGAG 1179
QY 376 LeuGlnGluArgAlaAspGluArgAlaArgLysMetLysLysHisGlyValLysPhe 395
Db 1180 TTTCAGAGAGCTGCTGATGAACGAGCGCAAAATGAACCG--CATGCTGTGAATTC 1236
QY 396 SerTrpIlePheAsnLysGluLeuLeu 405
Db 1237 AGCTGATTTTATATAAGAGATTATTTTG 1266

```

```

RESULT 4
LOCUS AY085086 1395 bp mRNA linear PLN 21-JUN-2002
DEFINITION Arabidopsis thaliana clone 12736 mRNA, complete sequence.

```

```

ACCESSION AY085086
VERSION AY085086.1 GI:21403796
KEYWORDS FLI CDNA.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 1395)
Haas, B.J., Volkovskiy, N., Town, C.D., Troukhan, M., Alexandrov, N.,
Feldmann, K.A., Flavell, R.B., White, O. and Salzberg, S.L.
Full-length messenger RNA sequences greatly improve genome
annotation
JOURNAL Genome Biol. (2002) In press
REFERENCE 2 (bases 1 to 1395)
AUTHORS Brover, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and
Feldmann, K.
Full-length cDNA from Arabidopsis thaliana
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 1395)
AUTHORS Brover, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and
Feldmann, K.
TITLE Direct Submission
COMMENT Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road,
Malibu, CA 90265, USA
This clone sequence is one of 5,000 Ceres full-length cDNAs made
available to TIGR and Genbank. The following quality assessment of
this set was done by comparison with known proteins: two percent
of the clones are estimated to be 5'-truncated; less than one percent
are 3'-truncated; approximately two percent represent alternative
splice variants, including unspliced introns and spliced exons; one
percent may contain premature stop codons; five percent may have
frame shifts in a coding region. A sequence is considered to be
5'-truncated if it lacks the translation initiation start (ATG). A
sequence is considered to be 3'-truncated if it lacks the
C-terminal end of the encoded protein. Please note that these cDNA
sequences are derived from the WS or Uder ecotypes and therefore
may contain polymorphisms when compared to sequences from Col-0.
GenSet carried out the library production and sequencing of the
full-length clones. Ceres, Inc. carried out the clustering of the
5' sequences, selection of clones, and sequence assembly.
FEATURES
source
location/Qualifiers
1..1395
/organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
/clone="12758"
48..1223
/codon_start=1
/product="stearyl acyl carrier protein desaturase,
putative"
/protein_id="AA061640.1"
/db_xref="GI:21537299"
/translational="MLTKSLSPPTOMATLMPSPFLASRRGPFAKTSAAVAPRP
AKHONKIHMPPEKMEIKESIDGNATDOLPLIKYDQWQASFLPALPESFT
DOYRELRNASLPDEFYVLVDKMTEDALPTQYMINILDSVREBTGASBAMASW
TRAWTAEENRHSGLRLPYLYLSGRVLMLEWERYQHLDSGMDPGTENNDYLGFTVTS
FDRATFESHGNTARLAKSAGDYLARICGTIADAKRHNAYRAIVKLEIDPNGA
VSAVADMRKRTKIMPAHLMGDGDPMLFEHFSVAORLEVTADVDADILEFVGMWR
LEKLEGLTGCGAORFVCGLAIRIRLDRADERAKKIKTKTHEVCFSMIFDQISV"
BASE COUNT 352 a 331 c 342 g 370 t
ORIGIN
Alignment Scores:
Pred. No.: 6,58e-111 Length: 1395
Score: 1466.00 Matches: 282
Percent Similarity: 82.35% Conservative: 40
Best Local Similarity: 72.12% Mismatches: 63
Query Match: 68.19% Indels: 6
DB: 8 Gaps: 2
US-09-934-900-2 (1-405) x AY085086 (1-1395)
QY 18 LysThrMetClnIleArgThrCysHisSerIleThrGlnThrLeuProGlnLeuPro 37

```

```

Db      45 AAAATGCTTACGACAAAGTCTTCTCTCTCCACCCACCAACCAATGGGTACACTAATGCA 104
Qy      38 CysSerSerArgLysAlaHisHisArgHisLeuProProLeuAsnAlaValSer 57
Db      105 TCTCCGCTCTACTTTTCTCGCTCTCGCCCGCGGACCGGCAAGATATGCGCGGTG--- 161
Qy      58 AlaAlaProPheLys-----AlaArgLysAlaHisSerMetProProGlu 72
Db      162 GCACACCTGTGAGCGCGGCTCTAAACACCAAAACAAATCCACACCATCCACCGAG 221
Qy      73 LysLysGluLeuPheLysSerLeuGluGlyThrPalaSerGluThrValLeuProLeu 92
Db      222 AAAATGAGATATTCAAATCTTTAGATGATGGCCACGATCAATCTTCGCTCTCTC 281
Qy      93 LysProValGluGlnGlyThrGlnProGlnAsnPheLeuProAspProSerLeuProHis 112
Db      282 AAACCCGTTGACCAATGTGGCAACCGCTTCTTTTACCCGACCGCGCTTACCCCTTC 341
Qy      113 GluGluPheSerHisGlnValLysGluLeuArgGluArgGlyThrLysGluLeuProAspGlu 132
Db      342 TCCAGATTACCGACCAAGTCTGTAGCTGAGGGAAGAAATGCGCTCCTCCAGACGA 401
Qy      133 TyrPheValValLeuValGlyAspMetValThrGluAspAlaLeuProThrTyrGlnThr 152
Db      402 TACTTCGTGTGTGTGTGTGAGATATGATTAACGAGAGCGGCTTGCCTACTTACACAGC 461
Qy      153 MetLeuAsnLeuAspGlyValLysAspAspSerGlyThrSerProSerProThrPala 172
Db      462 ATGTATCAACACCCCTGACGGCGTGAAGGACGACAGCTGTGAGTGAAGACGCGGCA 521
Qy      173 ValThrPheArgAlaThrPheAlaGluGluAsnArgHisGlyAspLeuLeuArgThrTyr 192
Db      522 AGTTGGACAAAGCGCTGACGCGTGAAGAGATGCTCATGTGATTTTTCGGGCTTAC 581
Qy      193 LeuTyrLeuSerGlyArgValAspMetAlaLysValGluLysThrValHisTyrLeuIle 212
Db      582 TTGTACTTATCCGGGCGTGTGATATGCTTATGTGTGAACGACCGCTTACACATCTATC 641
Qy      213 SerAlaGlyMetAspProGlyThrAspAsnAsnProTyrLeuGlyPheValTyrThrSer 232
Db      642 GGCTCGGGCATGATCTCCAGAACTGAGAACATCATCTAGAGTTTCTTACACGTCA 701
Qy      233 PheGlnGluArgAlaThrPheValAlaHisGlyAsnThrAlaArgLeuAlaLysGluLys 252
Db      702 TTCCAAGACGACCACTTTGTGTCTACGCAACAGCGGACGCTAGCCACGCGCA 761
Qy      253 GlyAspProValLeuAlaArgLeuGlyGlyThrIleAlaAlaAspGluLysArgHisGlu 272
Db      762 GGAGATCCTGTCTCGCTCGAATCTGCGGCAACATTCGACGTGACGAGAACGCCATGAA 821
Qy      273 AsnAlaTyrSerArgIleValGluLysLeuLeuGluValAspProThrGlyAlaMetVal 292
Db      822 AACCTTACGTAAGCATGCTGTGAGAAAGCTCTCGAGATGACCCCTAACGCGTCTCA 881
Qy      293 AlaIleGlyAsnMetMetGluLysLysIleThrMetProAlaHisLeuMetTyrAspGly 312
Db      882 GCCGTGGCGGACATGATCGGAGAGATCAATGCCGCTCATTAATGACAGACGCT 941
Qy      313 AspAspProArgLeuPheGluHisTyrSerAlaValAlaGlnArgIleGlyValTyrThr 332
Db      942 CGAGACCGCATGATTCGACATTTCTCCGCGGCTCAGCGGCTAGAGGTTTACAGC 1001
Qy      333 AlaAsnAspTyrAlaAspIleLeuGluPheLeuValGluArgTyrArgLeuGluLysLeu 352
Db      1002 GCGGATGATTCAGCTGACATCTTGAGATTTTGTGAGCAGCGTGAAGATTGAGAACTTA 1061
Qy      353 GluGlyLeuMetAlaGluGlyLysArgAlaGlnAspPheValCysGlyLeuAlaProArg 372
Db      1062 GAAGATTTGACGGGGAAGGCGCAACGTCACAGGAGTTTGTGTGGGTTAGCTAGAGG 1121
Qy      373 IleArgArgLeuGlnGluArgAlaAspGluArgAlaArgLysMetLysLysHisGly 392

```

```

Db      1122 ATTAGCGCCTTCAAGACCGTGCAGACGAGACGACTTAAGACTTAAGAACCCATGAG 1181
Qy      393 ValLysPheSerTrpIlePheAsnLysGluLeu 403
Db      1182 GTTGTCTTACTGTGATCTTGTGATTAAGCATG 1214
RESULT 5
ASU60277
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
BUILDING
FEATURES
SOURCE
5'UTR
CDS
transit_peptide
3'UTR
BASE COUNT
ORIGIN
Alignment Scores:
Pred. No.:
Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
US-09-934-900-2 (1-405) x ASU60277 (1-1284)
Qy      1 MetLeuSerIleIlePheLysGluPheValLysTyrAsnArgHisValIleLysThrMet 20
Db      1 CTTTGTCCATTAATTTGTAAC-----ACAGGAAAGAAAGAAAGAAAGTCTT 45
Qy      21 GlnIleArgThrCysHisSerIleThrThrGlnThrLeuProGlnLeuProCysSerSer 40

```

```

Db 46 -----GCACACGACCTTACCATGCAAACTTTC---GTATCTCCACCCCAAC 90
Qy 41 ArglyAlaHisArgHis-----LeuLeuProLeuAsnAlaVal 56
   |||  ::  |||  |||||  ::  |||||
Db 91 CCATCGCATGGAATGACATGGCTACCTATCAACACCCCAAAATCCACCGCTGA 150
Qy 57 -----SerAlaAlaProPheLysAlaArgLysAlaHis 67
   |||  |||  |||  |||  |||  |||
Db 151 TTCGGCCGACCTACCAACCTCTCCGGCGTAGCATCACCCAGCATGGCT----- 201
Qy 68 SerMetProGluLysArgLysGluLeuPheLysSerLeuGluLysTrpAlaSerGluTrp 87
   :::::  :::::  :::::  :::::  :::::  :::::
Db 202 ACATTGCGCCAGGAAAGATTCAAACTTTAGTCACTGAACTTGGGCGCAACCAAAAT 261
Qy 88 ValLeuProLeuLysArgValGluGlnCysTrpGlnProGlnAsnPheLeuProAsp 107
   |||||  |||||  |||||  |||||  |||||  |||||
Db 262 GTCCCTTCCCTTCTCAACCCCGTGTGGAATCATCATGCCAACCCAGAAATTCCTCCCGAAC 321
Qy 108 ProSerLeuProHisGluLysPheSerHisGlnValLysGluLeuArgLysGluTrpLys 127
   |||  ::  |||  ::  |||  ::  |||  ::  |||  ::  |||
Db 322 CCGGCTCAGAAATTTCCACGATTTCCACCAAGAAAGTTACAGCCCTCCGTCACCGTACCTCC 381
Qy 128 GluLeuProAspGluTrpPheValLysValLysPheMetValThrGlnLysAlaLeu 147
   :::::  :::::  :::::  :::::  :::::  :::::
Db 382 GATCTTCCCGATGAGTCTTGCTGCTTCTTGCGGACATGATTACGGAGAGACATTG 441
Qy 148 ProThrTrpGlnThrMetIleAsnAsnLeuAspGlyValLysAspAspSerGlyThrSer 167
   |||||  |||||  |||||  |||||  |||||  |||||
Db 442 CCAACTTATCAAGATGATTAACAGACTTGACGGCGTTAAGGATGACAGCGGAGCTTGT 501
Qy 168 ProSerProTrpAlaValTrpThrArgAlaTrpThrAlaGluLysAsnArgHisGlyAsp 187
   |||||  |||||  |||||  |||||  |||||  |||||
Db 502 ACTTCCCTTGGGCTATTGGACACAGCAGCTGGACGCGCGGAAGAAACCGTCACGCGCAT 561
Qy 188 LeuLeuArgThrTyrLeuTyrLeuSerGlyArgValLysMetAlaLysValGluTrpLys 207
   |||||  |||||  |||||  |||||  |||||  |||||
Db 562 TTACTCAACACTTATTTACCTTTCGCGACAGATTGACATGCAATGATGACAAACT 621
Qy 208 ValHisTyrLeuIleSerAlaGlyMetAspProGlyThrAspAsnAsnProTyrLeuGly 227
   ::  |||||  ::  |||||  ::  |||||  ::  |||||  ::  |||||
Db 622 ATCCAAATATTACTTACTCCGCGCATGACTGCTGCAAAATAGAAATCCGATTTGGA 681
Qy 228 PheValTyrThrSerPheGlnGluArgAlaThrPheValAlaHisGlyAsnThrAlaArg 247
   |||||  |||||  |||||  |||||  |||||  |||||
Db 682 TTGTGTACACGTCAATCCAGACGCGACATTTGTCTCACTGATGTAATCGGCTCG 741
Qy 248 LeuAlaLysGluGlyValAspProValLysAlaArgLysCysGlyThrIleAlaAlaAsp 267
   |||||  |||||  |||||  |||||  |||||  |||||
Db 742 CTCGCCAAGGAGAGAGGAGTCTGTCTAGTACCAATATGTGGTTCAATGCGATCGAC 801
Qy 268 GlyLysArgHisGlyAsnAlaTyrSerArgIleValGluLysLeuGluLysValAspPro 287
   |||||  |||||  |||||  |||||  |||||  |||||
Db 802 GAGAAGCGCCAGAGAGGCTTACTGAGAAATCGTGCAGAAATTAATGCGAAGTGGATCGG 861
Qy 288 ThrGlyAlaMetValAlaIleGlyAsnMetMetGlyLysIleThrMetProAlaHis 307
   :::::  :::::  :::::  :::::  :::::  :::::
Db 862 ACCGAGCGCATGTAGTCCATAGTGCATGATGAGAAATGAAATGCAATGCGCGCTCAT 921
Qy 308 LeuMetTyrAspGlyAspAspProArgLysPheGlnHisTyrSerAlaValAlaGlnArg 327
   |||||  |||||  |||||  |||||  |||||  |||||
Db 922 CTAAATGTACGAGCGCAAGATCCGAATCTGTTCGCTGCTTCCGCTTACCTCAACGA 981
Qy 328 IleGlyValTyrThrAlaAsnAspTyrAlaAspIleLeuGluPheLeuValGlnArgTrp 347
   :::::  :::::  :::::  :::::  :::::  :::::
Db 982 CTCGGGGTTTATACCTCCGAGACATTTATGCTGACATTTCTTGAATTTTAAATTCACCGTGG 1041
Qy 348 ArgLeuGluLysLeuGlnGlyLeuMetAlaGluLysArgAlaGlnAspPheValCys 367
   |||||  |||||  |||||  |||||  |||||  |||||
Db 1042 AGATTAGAGAAAGCTCGAGGGTTTGAAGATGAGAGAGCGTGCACAAAGATTCGCTGT 1101
Qy 368 GlyLeuAlaTrpArgIleArgArgLeuGlnGluAlaAspGluArgAlaArgLysMet 387
   |||||  |||||  |||||  |||||  |||||  |||||
Db 1102 GGACTAGTCTTAGATGAGGAGTTTACAAAGAAAGCTGACAGCGAGCCAAAGAGCTC 1161

```

```

Qy 388 LysLysHisHisGlyValLysPheSerTrpIlePheAsnLysGluLeuLeu 405
   :::::  :::::  :::::  :::::  :::::  :::::
Db 1162 CCGACACAGCATGAGATGAAATTTAGCTGACTTTAAATAGAGCTAATATTG 1215

RESULT 6
AX392322
LOCUS AX392322 1415 bp DNA linear PAT 23-MAR-2002
DEFINITION Sequence 11 from Patent WO0216565.
ACCESSION AX392322
VERSION AX392322.1 GI:19700685
KEYWORDS
SOURCE
ORGANISM
Zea mays.
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogonae; Zea.

REFERENCE
AUTHORS 1
TITLE Booth, J.R., Cahoon, R.E., Hitz, W.D., Kinney, A.J. and Yadav, N.S.
JOURNAL Nucleotide sequences of a new class of diverged delta-9
stearyl-acp desaturase genes
Patent: WO 0216565-A 11 28-FEB-2002;
E. I. du Pont de Nemours and Company (US)
FEATURES
source Location/Qualifiers
1..1415
/organism="Zea mays"
/db_xref="taxon:4577"

BASE COUNT 249 a 476 c 472 g 218 t
ORIGIN

Alignment Scores:
Pred. No.: 1,84e-100 Length: 1415
Score: 1338.50 Matches: 262
Percent Similarity: 76.09 Conservative: 53
Best Local Similarity: 63.29 Mismatches: 69
Query Match: 62.26 Indels: 30
Gaps: 5

US-09-934-900-2 (1-405) x AX392322 (1-1415)
Qy 19 ThrMetGlnIleArgThrGlyHisSerIleThrGlnThrLeuProGlnLeuProCys 38
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 21 ACAGAGCTGTCGCGGCTCCACTCCACAGTACCCACCGCGCTCTCCAGGCTCCGCGC 80
Qy 39 SerSerArgLysAla-----HisHisArgHis----- 47
   ::  ::  ::  ::  ::  ::  ::  ::  ::  ::
Db 81 CGTACGCGCGGACGACCAACCGAGCGGACAGTGCAGCGCCACGGATGCGCATCGCGC 140
Qy 48 -----LeuLeuProLeuAs 53
   :::::  :::::  :::::  :::::  :::::  :::::
Db 141 CCGCGGCGCGGTGGCGCGGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGCTGC 200
Qy 53 nAlaAlaValSerAlaAlaProPheLysAlaArgLysAlaHisSerMetProGluLys 73
   |||||  |||||  |||||  |||||  |||||  |||||
Db 201 GCGCGGCGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGAA 260
Qy 73 LysGluIlePheLysSerLeuGluLysTrpAlaSerGluTrpValLeuProLeuLys 93
   |||||  |||||  |||||  |||||  |||||  |||||
Db 261 GCGGAGAGCTTCCGCTGCTGGAAGGCTGGGCGGCGGCGGCGGCTGCTGCTGCTGCA 320
Qy 321 sPProValGluGlnCysTrpGlnProGlnAsnPheLeuProAspProSerLeuProHisG 113
   |||||  |||||  |||||  |||||  |||||  |||||
Db 93 sPProValGluGlnCysTrpGlnProGlnAsnPheLeuProAspProSerLeuProHisG 113
   |||||  |||||  |||||  |||||  |||||  |||||
Db 321 GCGCGGAGAGAGTGGTGGCACCGGAGACTTCTCCCGGAGCTCTG-----TCCGA 374
Qy 113 uGluPheSerHisGlnValLysGluLeuArgGluArgThrLysGluLeuProAspGluLys 133
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 375 GATGTTCCGGGACAGAGTCCGCGAGCTGCGCCCGCGCGCGGCGGCTCCCGAGAGGA 434
Qy 133 rPheValValLeuValLysAspMetValThrGlnAspAlaLeuProThrTyrGlnIle 153
   |||||  |||||  |||||  |||||  |||||  |||||
Db 435 CTCGCTGCTGCTGCTGCGGACATGCTCAGGAAGGCGGCTGCGCCAGCTACCAAGACT 494
Qy 153 tIleAsnAsnLeuAspGlyValLysAspAspSerGlyThrSerProSerProTrpAlaVal 173

```

```

Db 495 GATCAACACAGCTCGACGGCGTCTCGGACGAGACCGCCGACCACTGCGCCCTGGCGCGT 554
Qy 173 LTPHTRARGALATPHTHRAAGLUGLUAASNRHISGLYSPLLEULEUATGTHTYLLE 193
Db 555 CTGGACGGCGCCCTGGAGCCCGGAGAGAACCGCCGACACACCTCCGCGCAAGTACAT 614
Qy 193 UTITRUSERGLYARGVALASPMETALALVALGLUYSRTHVALHISTYRLEULISE 213
Db 615 GTACCTATCCGGCCCGCGTCCGACATCCGATGTCAGAGAACCGTCCAGTACCTATCGG 674
Qy 213 FALAGLYMETASPPROGLYTHRASPSANSPROTYRLEUALLYPHEVALTYRTHSERPH 233
Db 675 CTCGGCGCATGATCCCGGAGACGAGAACACCCGACTGCGGCTTCGTGTACAGACGCTT 734
Qy 233 EGLGLUARGALATPHTHRAAGLUGLUAASNRHISGLYSPLLEULEUATGTHTYLLE 253
Db 735 CCAGGAGCGCGCGCGCGTCTCGGACGAGAACCGCCGCGCGTCCGCGCACGCG 794
Qy 253 YASPPROVALLEUALAATRGLEUCYGLYTHRTLEALALASPSGLUYSARGHISGLUAS 273
Db 795 GGAGAGACTCTCTGGCGCGCGCTCGGACCATCGCCCGACGAGAACGCGCACGAGAC 854
Qy 273 NALATYRSEARGLLEVALGLUYSLEULEUGLUALASPPROTHRGILALAMETVALAL 293
Db 855 GCGCGTACGCGCATCTCGAGACAGCTCTGACAGTGGACCGGAGCGCGCGTCTCGC 914
Qy 293 ALLEGLYSMETMETGLUYSLYSILETHMETPROALAHISLEUMETTYRASGLYAS 313
Db 915 CGTGGCGGACATGATGCGCAAGCGGATCACCATCGCCCGCACCTCATGACAGCGCGG 974
Qy 313 PASPPROARGLEUPHEGLUHISTYRSEARALVALAAGLARGILEGLYVALTYRTHAL 333
Db 975 CGACATGACACTGTTCCGAGCACTTCGCCCGCGCGCGCTCCGCGGTACACCGCC 1034
Qy 333 AASNASPTYRALAASPLEULEUGLUPHELEUVALGLUARGTPARGLEUGLULYSLEUL 353
Db 1035 CCGGGACTACCGCGCATCTCGAGTCTCTGTCAAGGGGAGGAGCTGAGACACTGSA 1094
Qy 353 U---GLYLEUMETALAGLUGLULYSARGALAGLNASPHEVALCYSGLYLEUALAPROAR 372
Db 1095 GAGCGGCTCTCCGCGGAGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1154
Qy 372 GLEARGARGLEUGLUGLARGALAAASPLUARGLARGLYSMETLYSHLSHLSGL 392
Db 1155 GATGCGCGCGCGCGCGGAGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1211
Qy 392 YALLYSPHESERTPRILEPHASNLYSGLULEULEU 405
Db 1212 GGTCAAGTTCAAGTGTGATCTTGATAGGAGGAGCGTGT 1251

RESULT 7
LOCUS TA007597 1337 bp mRNA linear PLN 26-JAN-1995
DEFINITION Thunbergia alata clone pTAD2 delta-9 stearyl-acyl carrier protein
desaturase precursor mRNA, complete cds.
ACCESSION U07597
VERSION U07597.1 GI:533083
KEYWORDS
SOURCE
ORGANISM
Thunbergia alata.
Thunbergia alata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; eustersids I; Lamiales; Acanthaceae; Thunbergia.
REFERENCE
1 (bases 1 to 1337)
Cahoon,E.B., Becker,C.K., Shanklin,J. and Ohlroge,J.B.
desaturase from Thunbergia alata endosperm
Plant Physiol. 106 (2), 807-808 (1994)
JOURNAL MEDLINE
95083771
7991701
REFERENCE
2 (bases 1 to 1337)
Cahoon,E.B.

```

```

TITLE Direct Submission
JOURNAL Submitted (08-MAR-1994) Cahoon E. B., Brookhaven National
Laboratory, Biology, Upton, NY 11973, USA
FEATURES
source
1..1337
/organism="Thunbergia alata"
/db_xref="taxon:32198"
/clone="pTAD2"
/note="authority=Bojer ex Sims"
37..1209
/EC_number="1.14.99.6"
/codon_start=1
/evidence-experimental
/product="delta-9 stearyl-acyl carrier protein desaturase
precursor"
protein_id="AA061559.1"
/db_xref="GI:533084"
/translation="MALKCVTPHQVSPFVYNOLRSRHYVASTLDSASANGKGRKA
FTPPREVVOLTHPMAPKREIFSHLSHGMANENLISLKPVKCMOPNDPLPDSSEG
FDEOYRELRLRTKELPDYEFVYLVGDMTEALPYOTMINTLAVRETCASLTPMA
IWTBMTAEENRHGDLNKYILXISGRVDMROIEKTIQYLISGMDPRDNPYLGFTY
TSFORATFISHGNTARLAKHGDILKALQIGSLNADKRHEHATKLTIERLFEDPD
GTVALADMMRKVSMFPAHLMDQDENLFEHFAVAQRIGVYTRAKDVALILELVGR
WEVKLTGLSGEGRNAOEYVGLAPRIRLREBRAQARAKOGAPVFFSWYGREVYI"
transit_peptide 37..117
mat_peptide
118..1206
/product="delta-9 stearyl-acyl carrier protein
desaturase"
/EC_number="1.14.99.6"
/function="oleic acid synthesis"
/standard_name="delta-9-18:0-ACP desaturase"
/evidence-experimental
1337
/note="18 A residues"
BASE COUNT 361 a 293 c 339 g 344 t
ORIGIN
polyA_site
Alignment Scores:
Pred. No.: 2,276-100 Length: 1337
Score: 1337.00 Matches: 251
Percent Similarity: 78.41% Conservative: 54
Best Local Similarity: 64.52% Mismatches: 66
Query Match: 62.19% Indels: 18
Gaps: 4
US-09-934-900-2 (1-405) x TA007597 (1-1337)
Qy 27 SerIleRrThrGlnThrLeuProGlnLeuProCysSerSerArgLysAlaHisHisArg 46
Db 52 AGCGTAACCCCCCAGGAGTGGCTCTTCTCTGTATACAGCTCAGATTCACCGAGGT 111
Qy 47 HisLeuLeuProProLeuAsnAlaAlaValSerAlaAlaProPheLysAlaArgLysAla 66
Db 112 TACATGGCTTCAACTCTGATTCGATTCGCA---TCCGCTAATGTTGGAGAAAGTAAAAAGCT 168
Qy 67 -----HisSerMetProProGlnLysLys 74
Db 169 TTCACCCCCCTCGAAGAGTCAGAGTTCACTGACGCAATCCCATGCTCTCGAAGAGCGC 228
Qy 75 GluIlePheLysSerLeuGluGlnYrPrpAlaSerGlnYrValLeuProLeuLysPro 94
Db 229 GAGATCTTCATTACTCGACAGGTTGGGCGGAGAAACCTTCGTCTCTTGAAGCT 288
Qy 95 ValGluGlnCysTTrpGlnProGlnAsnPheLeuProAspProSerLeuProHisGluGlu 114
Db 289 GTTGAAGAGTGTGGACCCCAAGCACTTCTTCCCGACCTTC-----TCAGAAAGC 342
Qy 115 PheSerHisGlnValLysGluLeuArgGluArgThrLysGluLeuProAspGluYrPhe 134
Db 343 TTTCATGAACAGGTAGGAGCTTGGCTAACAGCAAGAGACTACCGATGAATACTTT 402
Qy 135 ValValLeuValGlyAspMetValThrGlnLysPalaLeuProThrTyrGlnThrMetIle 154

```

Db 403 GTTGTGTTGGGACATGATCAGGAGAACGCTCTCCACTTATATACAGATGATC 462  
 Qy 155 AaanaLeuaspGlyValLysaspSerGlyThrSerProSerProThrAlaValTrp 174  
 Db 463 AACACTTAGATGATCCGATGATGAGACCGGATGACAGCCTTACTCTGGGCTATTGG 522  
 Qy 175 ThrArgAlaThrPheValAlaHisGlyAsnArgHisGlyAspLeuArgThrTyrluYr 194  
 Db 523 ACTAGAGCATGAGCCGAGAGAAATAGACAGCGGATCTCTCAAAAATATCTTTAC 582  
 Qy 195 LeuSerGlyArgValAspMetAlaLysValGlyLysThrValHisTyrluLeuSerAla 214  
 Db 583 CTTTGGGACCGCTGACATGAGCAATTCAGAACATTCATCACTCATCGGTTA 642  
 Qy 215 GlyMetAspProGlyThrAspAsnProTyrluGlyPheValTyrluThrSerPheGln 234  
 Db 643 GGAATGATCTCTGCGACGATTAACAACCGTACCTCGATCATACACCTGTTCCAG 702  
 Qy 235 GluArgAlaThrPheValAlaHisGlyAsnThrAlaArgLeuAlaLysGluGlyAsp 254  
 Db 703 GAGAGGCGACATTCATTTCTCATGGAAACAGCGCTGAGCTTCCAAAGAACACGGGAC 762  
 Qy 255 ProValLeuAlaArgLeuGlySerGlyThrIleAlaAlaAspGlyLysArgHisGluAsnAla 274  
 Db 763 CTTAAATCTGCAAGATATGCGCAGCATAGCTGAGATGAGAAACGACGAACTGCT 822  
 Qy 275 TyrSerArgIleValGlyLysLeuGluValAspProThrGlyAlaMetValAlaIle 294  
 Db 823 TACACCAAAATATGCGAAAGCTGTTGATGATGACCCGATGCGGACATGACTGCTCA 882  
 Qy 295 GlyAsnMetMetGlyLysIleThrMetProAlaHisLeuMetTyrluAspGlyAsp 314  
 Db 883 GCGGATATGATGAGGAAAGTGTCTATGCGCGCACATTTGATGATGATGACAAAGAT 942  
 Qy 315 ProArgLeuPheGlyHisTyrluSerAlaValAlaGlnArgIleGlyValTyrluThrAlaAsn 334  
 Db 943 GAAATCTCTTGGAACTTTCGACCTGCGCGCAACGATGAGTGTACCTGCGAAA 1002  
 Qy 335 AspTyrluAlaAspIleLeuGluPheLeuValGluArgTyrluArgLeuGluLysLeuGluGly 354  
 Db 1003 GACTATGCTGATATCTGAAATTTTATGTTGGAGATGGAGGTGAGAACTACACAGA 1062  
 Qy 355 LeuMetAlaGluGlyLysArgAlaGlnAspPheValCysGlyLeuAlaProArgIleArg 374  
 Db 1063 CTTTCAGGGAGGGTGTACACCGCAGGAGTACGTGCGGTGCTGCTCGGATCAGA 1122  
 Qy 375 ArgLeuGlnGluArgAlaAspGluArgAlaArgLysMetLysLysHisGlyValLys 394  
 Db 1123 AGGTTGGAAGAGACACAGCAGCAGGCA-----AGCAGGGGGCACCTGTGCC 1173  
 Qy 395 PheSerTrpIlePheAsnLysGluLeu 403  
 Db 1174 TTCTCCTGGGTTTATGCTGAGAAAGTT 1200  
 RESULT 8  
 AX392326  
 LOCUS AX392326 1318 bp DNA linear PAT 23-MAR-2002  
 DEFINITION Sequence 15 from Patent WO0216565.  
 ACCESSION AX392326  
 VERSION AX392326.1 GI:19700687  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Oryza sativa.  
 Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhacoidae; Oryzeae; Oryza.  
 REFERENCE  
 AUTHORS Booth, J. R., Cahoon, R. E., Hitz, W. D., Kinney, A. J. and Yadav, N. S.  
 TITLE Nucleotide sequences of a new class of diverged delta-9  
 steroyl-acp desaturase genes  
 JOURNAL Patent: WO 0216565-A 15 28-FEB-2002;  
 E. I. du Pont de Nemours and Company (US)  
 FEATURES  
 Location/Qualifiers

source 1.1318  
 /organism="Oryza sativa"  
 /db\_xref="taxon:4530"  
 BASE COUNT 248 a 402 c 451 g 217 t  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 3,43e-99 Length: 1318  
 Score: 1322.50 Matches: 253  
 Percent Similarity: 78.01% Conservative: 52  
 Best Local Similarity: 64.71% Mismatches: 73  
 Query Match: 61.51% Indels: 13  
 DB: 6 Gaps: 4  
 US-09-934-900-2 (1-405) x AX392326 (1-1318)  
 Qy 16 ValIleLysThrMetGlnIleArgThrCysHisSerIleThrThrGlnThrLeuProGln 35  
 Db 54 GTCTGGGAAACGCTGCTCAGTGGCTCGCGCGGCTGCGCGCCCTCGCGCGCGAG 113  
 Qy 36 LeuProCysSerSerArgLysAlaHisArgHisLeuLeuProLeuAsnAlaAla 55  
 Db 114 TCCGCGGTGTCGCG-----GCGGTGCTGACGGCGCG 146  
 Qy 56 ValSerAlaAlaProPheLysAlaArgLysAlaHisSerMetProProGluLysGlu 75  
 Db 147 GAGAGCGCAGCGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 206  
 Qy 76 IlePheLysSerLeuGlnGlyThrAlaSerGluTyrValLeuProLeuLysProVal 95  
 Db 207 GTGTTCGGTCTCTGAGAGGGTGGGAGCGTGTCTCTCGCTCTCGCTCTCAAGCCGTG 266  
 Qy '96 GluGlnCysTrpGlnProGlnAsnPheLeuProAspProSerLeuProHisGluIlePhe 115  
 Db 267 GAGAGTGTGTCAGCGCAGCGCAGCGACCTCTCGCGCGACTGCTG-----TCGAGATGTTTC 320  
 Qy 116 SerHisGlnValLysGluLeuArgGluArgThrLysGluLeuProAspGluTyrluPheVal 135  
 Db 321 GAGCAGCAGGTCCAGACGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGTTC 380  
 Qy 136 ValLeuValAlaAspMetValThrGluAspAlaLeuProThrTyrluThrMetIleAsn 155  
 Db 381 GTGCTGTGCGGGACATGTTTACCGAGAGGGCGTCCGACCTACCAAGCATGATCAAC 440  
 Qy 156 AsnLeuAspGlyValLysAspSerGlyThrSerProSerProThrAlaValTrpThr 175  
 Db 441 ACGCTCGAGCGGCTCGCGCAGAGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 500  
 Qy 176 ArgAlaThrThrAlaGluGluAsnArgHisGlyAspLeuArgThrTyrluTyrluYr 195  
 Db 501 CCGACCTGACCGCGCGAGAGAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTTC 560  
 Qy 196 SerGlyArgValAspMetAlaLysValGlyLysThrValHisTyrluLeuLeuSerAlaGly 215  
 Db 561 TCCGCGCGCTGACATGCGCATGCTGCGAGAGACCGTCACTACCTCATCGGCTCCGCG 620  
 Qy 216 MetAspProGlyThrAspAsnProTyrluGlyPheValTyrluThrSerPheGlnGlu 235  
 Db 621 ATGATCCGCGGAGAGAAACCGCTACGCGGTTCTGTACACACGCTTCCAGAGAG 680  
 Qy 236 ArgAlaThrPheValAlaHisGlyAsnThrAlaArgLeuAlaLysGluGlyLysPro 255  
 Db 681 CCGCGGAGCGCGCTGCGCGAGAACAGCGCGCGCGCGCGCGCGCGCGCGCGCGAGC 740  
 Qy 256 ValLeuAlaArgLeuGlySerGlyThrIleAlaAlaAspGluLysArgHisGluAsnAlaTyrlu 275  
 Db 741 GTCTGCGCGCGCACTGCGGCACTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTAC 800  
 Qy 276 SerArgIleValGlyLysLeuGluValAspProThrGlyAlaMetValAlaIleGly 295  
 Db 801 GGGCGATCGTGAGAGAGCTGCTGCGGCTGACCGCGAGCGCGCGCATGCTCGCATCGCC 860  
 Qy 296 AsnMetMetGluLysIleThrMetProAlaHisLeuMetTyrluAspGlyAspPro 315

```

Db      861 GACATGATGCACAGCGATCACATGCCCGCCACCTCATGCAGACGCGCCGACATG 920
      316 ArgLeuPheGluHisIySerAlaValAlaGlnArgIleGlyValIyThrAlaAsnAp 335
      921 AACCTGTGACCACTTCCGCGCGCGCGACCGCTCACGCTCACCGCGCCGCGAC 980
      336 TyrAlaAspIleLeuGluPheLeuValAlaGlyTrpArgLeuGluIyLysLeuGlu 354
      981 TACGCCGACATGCTGCAGTCTCTCCGACAGCGGTGAGACCTGAGACCTGGAGACTGG 1040
      355 LeuMetAlaGluGlyLysAlaGlnAlaGlnAspPheValCysGlyLeuAlaProArgIleArg 374
      1041 CTCTCCGCGCGAGCGCGCGAGCGCGCGGACTTCGTGTGCGGCTCGCAAGAGGATCGCG 1100
      375 ArgLeuGlnGluArgAlaAspGluArgAlaGlyLysMetLysHisIleGlyValLys 394
      1101 CGGCGCGCGCGCGCGCTGAGACAGCGCTGAGAG--GATGAGCAGAGAGAGGTCAG 1157
      395 PheSerTrpIlePheAsnLysGluLeuLeuLeu 405
      1158 TTCACGTGATATGATGATGAGGAGATGATTGTC 1190

RESULT 9
SMNSCPD      1576 bp  mRNA  linear  PLN 27-APR-1993
LOCUS      Simmondsia chinensis stearoyl-acyl carrier protein desaturase mRNA,
DEFINITION  complete cds.
ACCESSION  M83199.1 GI:169894
VERSION  M83199.1 GI:169894
KEYWORDS  stearoyl-acyl carrier protein desaturase.
SOURCE  Simmondsia chinensis embryo immature seed cDNA to mRNA.
ORGANISM  Simmondsia chinensis
Eukaryota; Vitidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllidae; Caryophyllales; Simmondsiaceae; Simmondsia.
1 (bases 1 to 1576)
Sato,A., Becker,C.K. and Knauf,V.C.
Nucleotide sequence of a complementary DNA clone encoding
stearoyl-acyl carrier protein desaturase from Simmondsia chinensis
Plant Physiol. 99, 362-363 (1992)
JOURNAL
FEATURES
source
1.1576
/organism="Simmondsia chinensis"
/db_xref="taxon:3999"
/tissue_type="immature seed"
/dev_stage="embryo"
1.1576
/gene="stearoyl-acyl carrier protein desaturase"
98..1294
/gene="stearoyl-acyl carrier protein desaturase"
/BC_number="1.14.99.6"
/codon_start=1
/product="stearoyl-acyl carrier protein desaturase"
/protein_id="AAA33932.1"
/db_xref="GI:169895"
/translation="MALIKHTAFNPSMAVTSSGLPRSHLSHRFYMASSRTIGTISK
ETPNAKPMPPREAHVQKTHSPAPKIEFSLSGMAEENLVHLKPEKQWQPDF
LDPDASEGFMQVKELEKERTKEIPDEYLVLVGDMLTEALPYQYMLTLDGVDET
GASLTSMATWTRAMTAENRHDILNKYLYLGRVDMKQIEKTIQYLLISGMDPRSEN
NPYLGTYSFOERATFISGNTARLAKQHPOLAOVCGIITAAADKREHETATKIVE
KLEFDPDGAVLADDMRKYSMPAHMLWDKNDLFPNYSVAVNOOITVYRAKQYAD
ILEHLINRKRKVENKMLSGEHRKADDFVCGLARIRIKLEBRQSLSPVSPFSMT
NKLKY"
transit_peptide 98..199
/gene="stearoyl-acyl carrier protein desaturase"
mat_peptide 200..1291
/gene="stearoyl-acyl carrier protein desaturase"
/product="stearoyl-acyl carrier protein desaturase"
/BC_number="1.14.99.6"
1576
polyA_site /gene="stearoyl-acyl carrier protein desaturase"
BASE COUNT 453 a 361 c 356 g 406 t

```

```

ORIGIN
Alignment Scores:
Pred. No.: 1,22e-98 Length: 1576
Score: 1317.00 Matches: 250
Percent Similarity: 80.32% Conservative: 52
Best Local Similarity: 66.49% Mismatches: 54
Query Match: 61.26% Indels: 20
DB: 8 Gaps: 5

US-09-934-900-2 (1-405) x SMNSCPD (1-1576)
      28 ILeThrThGlnThrLeuProGluLeuProCysSerSerArgLysAlaHisIleArgHis 47
      218 ATTACTTCTAAGAGATFACC-----AATGCCAAAAGCCTC----- 256
      48 LeuLeuProProLeuAsnAlaAlaValSerAlaAlaProPheLysAlaArgLysAlaHis 67
      257 ---ATGCTCTCAGAGACCTCATGTG-----CAANAAGCCAT 292
      68 SerMetProProGluLysGluLysIlePheLysSerLeuGluGlyTrpAlaSerGluTrp 87
      293 TCAMTCCCGCCCAAAAGATTGAGATTTCAAATCCCTTGAGAGGTGGCTGAGGAGAT 352
      88 ValLeuProLeuLeuLysProValGluGlnCysTrpGlnProGluAsnPheLeuProAsp 107
      353 GCTTGTGTCATCTTAACCTGTGGAGAGGTGGCAACACAGATTCTTACCCGAC 412
      108 ProSerLeuProHisGluGluPheSerHisGlnValLysGluLeuArgGluArgTrpLys 127
      413 CGGCGC-----TCCAGGAGATTATGATCAAGTCAAGAGATTGAGGAAAGAACCA 466
      128 GluLeuProAspGluTrpPheValAlaValLeuValGlyAspMetValThrGluAspAlaLeu 147
      467 GAATCCCGGATGAGTACCTTGTGGTGGTGGGAAATGATCTACTAAGAAAGTCTT 526
      148 ProThrTrpGlnThrMetIleAsnLeuAsnLeuAspGlyValLysAspSerGlyThrSer 167
      527 CCGACCTTACAGACGATGCTTAAACGCTCGATGAGGATGATGATGACGGTGCACG 586
      168 ProSerProTrpAlaValTrpThrArgAlaTrpThrAlaGluGluAsnArgHisGlyAsp 187
      587 CTTACTTCTTGGGCTATCTGAGACCGCGCATGAGCGCTGAGAGATAGGACGCGTAT 646
      188 LeuLeuArgThrIyLeuTrpIyLeuSerGlyArgValAlaAspMetAlaLysValGlyTrp 207
      647 CTTTGAACAAAGTATCTTAACTTACTGTGCGATGACATGATGAGAGAGACACA 706
      208 ValHisTrpLeuIleSerAlaGlyMetAspProGlyThrAspAsnAsnProTrpLeuGly 227
      707 ATCCAGTATCTTAATCGAGTCTGAGATGAGACCTCGAAGTGAACAAACCCCTATCTTAGG 766
      228 PheValIyTrpThrSerPheGlnGluArgAlaTrpPheValAlaHisGlyAsnThrAlaArg 247
      767 TTCATCTACACTCTCTTCAAGAGAGACCACTTCATCCCATGGAACACGCGTAGG 826
      248 LeuAlaLysGluGlyLysAspProValLeuAlaArgLeuGlySerGlyThrIleAlaAlaAsp 267
      827 CTTCGCAAAAGACACGCGCTTCAACATGACCAAGTATGTGGCATCATCGGTGAGAT 886
      268 GluLysArgHisGluAsnAlaTrpSerArgIleValGluLysLeuLeuGluValaAspPro 287
      887 GAGAACCGCCACCAAACTGCTTACACAAAATTTGTGAAAAGCTCTTTGAATCGACCCA 946
      288 ThrGlyAlaMetValAlaIleGlyAsnMetMetGluLysLysIleThrMetProAlaHis 307
      947 GACGGCGCTGTCTTACACACTGACATGATGATGAGAAAGAGTTTCCATGCCAGCCAC 1006
      308 LeuMetLysAspLysAspAspProArgLeuPheGluHisIySerAlaValAlaGlnArg 327
      1007 TTATGTATGATGATGCAAGATGCAATCTTGTGAGAACATACACACCGCTCGTCAACA 1066
      328 IleGlyValIyTrpThrAlaAsnAspTrpAlaAspIleLeuGluPheLeuValGluArgTrp 347

```

```

|||||
Db 1067 ATGGAGTTTACCCCGAAGGACTGACGATCCTCGACACCTCGTTAATCCCTGG 1126
QY 348 ArgLeuGluLysLeuGluLeuMetAlaGluGlyLysArgAlaGlnAspPheValCys 367
Db 1127 AAGTCGACAAATTAATGGCTGTCTGCGCGAGGACATTAAGCTCAAGATTCTGTATGT 1186
QY 368 GlyLeuAlaProArgIleArgArgLeuGlnGluArgAlaAspGluArgAlaArgLysMet 387
Db 1187 GGGTTGGCCCCGAGATCAGAAACCTCGGGAGAGAGAGCTCAGTCGGTACCAACGCGTA 1246
QY 388 LysLysHisHisGlyValLysPheSerTrpIlePheAsnLysGluLeu 403
Db 1247 TCTCTT-----GTCCCTTCACGCTGATTTTCACACGAAATG 1285

RESULT 10
TAU07605 1443 bp mRNA linear PLN 26-JAN-1995
DEFINITION Thumbergia alata clone pRAD3 delta-9-stearoyl-acyl carrier protein
ACCESSION U07605
VERSION U07605.1 GI:533085
KEYWORDS Thumbergia alata.
SOURCE Thumbergia alata.
ORGANISM Thumbergia alata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; easterids I; Lamiales; Acanthaceae; Thumbergia.
1 (bases 1 to 1443)
Cahoon,E.B., Becker,C.K., Shanklin,J. and Ohlrogge,J.B.
cDNAs for isoforms of the delta 9-stearoyl-acyl carrier protein
desaturase from Thumbergia alata endosperm
Plant Physiol. 106 (2), 807-808 (1994)
JOURNAL 95083771
MEDLINE 7991701
PUBMED 2 (bases 1 to 1443)
REFERENCE Cahoon,E.B.
AUTHORS Direct Submission
TITLE Submitted (08-MAR-1994) Cahoon E. B., Brookhaven National
JOURNAL Laboratory, Biology, Upton, NY 11973, USA
FEATURES
source
1. 1443
/organism="Thumbergia alata"
/db_xref="taxon:32198"
/clone="pRAD3"
/tissue_type="endosperm"
/clone_lib="Lambda ZAPII (Uni-ZAP XR) cDNA expression
library"
/dev_stage="postpollination"
/note="authority=Bojer ex Sims"
56..1228
/EC_number="1.14.99.6"
/codon_start=1
/evidence=experimental
/product="precursor delta-9-stearoyl-acyl carrier protein
desaturase"
/protein_id="AAA61560.1"
/db_xref="GI:533086"
/translation="MALKRSIPKMKSPRPDQLSRHYCMSTLYSASVEYNGKKP
FSPREVNIOVTHMPPEKREIFNSLHGAETNLSLTPVDKQPSPLDPDSADG
FEDQVRELKRTKELDEYFVILIGMTIEALPYOTINILDAVRDGTGSLTEWA
INNRWATAEENRHDGLNKLKYLISGRVDMKQVEKTYQYLISGMDPHTNPNLYGFIY
TSFERATFISGNTFARLAKERHDMKLAICGTIADERHETAYRKIIKLEFLDPPD
GTLIALADMKRKVSMFAHLMFDGKDONLFERSAVAORLIGVYTAADYADILEYVAR
WEVEKTLGILGSRKAQEVYCGIAPRIRLDERAQRARAKAAPVPTTWLFGREVR."
transit_peptide 56..136
mat_peptide 137..1225
/product="delta-9-stearoyl-acyl carrier protein
desaturase"
/EC_number="1.14.99.6"
/function="oleic acid synthesis"
/standard_name="delta-9-18:0-ACP desaturase"
/evidence=experimental

```

```

polya_site 1443
BASE COUNT 416 a 294 c 347 g 386 t
ORIGIN
Alignment Scores: 2,31e-98 Length: 1443
Pred. No.: 1313.00 Matches: 247
Score: 77.44% Conservative: 55
Percent Similarity: 63.33% Mismatches: 72
Best Local Similarity: 61.07% Indels: 16
Query Match: 8 Gaps: 5
DB: 8

US-09-934-900-2 (1-405) x TAU07605 (1-1443)
QY 27 SerIleThrThrIleThrIleProGlnLeuProCysSerSerArgLysAlaHisIleArg 46
Db 71 AGCATTACGCCGCCACAGATGCTCTCTCCCTCGATTCCAGCTCAGATCTACCGGGTT 130
QY 47 HisLeuLeuProProLeu--AsnAlaAlaValSerAlaAla-----ProPhe 61
Db 131 TGCATGACTTCACACTCTCTATTCTGATCTGATCCGTTGAGGTGGCAATGTAAGCCTTTC 190
QY 62 LysAlaArgLys-----AlaHisSerMetProProGluLysGlu 75
Db 191 AGTCCCCCTCGAGAAAGTCAATATTCAAGTGACACATCCATGCTCCAGAAAGCCGAG 250
QY 76 IlePheLysSerLeuGluGluGlyTrpAlaSerGluTrpValLeuProLeuLysProVal 95
Db 251 ATCTTAACCTCATTCGATGGATGGATGGCGGAAACATATCTCTCTCTTGAAGCCTGTT 310
QY 96 GluGlnCysTrpLeuProGlnAsnPheLeuProAspProSerLeuProHisGluGluPhe 115
Db 311 GACAAAGTGTGGAGCCAGCTGACTTTCACCGACCCCTCCGCA-----GATGGCTTT 364
QY 116 SerHisGluValLysLeuLeuArgGluArgGlyLysGluLeuProAspGluTrpPheVal 135
Db 365 GAGCAGCAGCTCGAGAGTTCAGGAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 424
QY 136 ValLeuValGlyAspMetValTrpGluAspAlaLeuProThrTyrGlnThrMetIleAsn 155
Db 425 GTGTTATTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
QY 156 AsnLeuAspGlyValLysAspAspSerGlyThrSerProSerProTrpAlaValTrpThr 175
Db 485 ACCGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 244
QY 176 ArgAlaTrpThrAlaGluGluAsnArgHisGlyAspLeuLeuArgThrTyrLeuTyrLeu 195
Db 545 AGAGCATGAGCTCTCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 604
QY 196 SerGlyArgValAspMetAlaLysValGluLysValHisIleTyrLeuIleSerAlaGly 215
Db 605 TCGGAGCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 664
QY 216 MetAspProGlyThrAspAsnAsnProTyrLeuGlyPheValTyrThrSerPheGlnGlu 235
Db 665 ATGAGCCGTCATCATGATAAACCCTGATCCTGATGATGATGATGATGATGATGATGATGAT 724
QY 236 ArgAlaTrpPheValAlaHisGlyAsnThrAlaArgLeuAlaLysGluLysGluAspPro 255
Db 725 AGAGCAACATTCATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 784
QY 256 ValLeuAlaArgLeuGluGlyThrIleAlaAlaAspGluLysArgHisGluAsnAlaTyr 275
Db 785 AAATCGCACAGATTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 844
QY 276 SerArgIleValGluLysLeuLeuGluValAspProThrGlyAlaMetValAlaIleGly 295
Db 845 ACAAATAATTAATGAAGCTGTTTACGTGAGACCGCTGATGATGATGATGATGATGATGAT 904
QY 296 AsnMetMetGluLysLysIleThrMetProAlaHisLeuMetLysArgLysAspAspPro 315

```

QY	Db	905	GACATGATGCGGAGAAAGTGTGCATGGCTGCCACACGATGCTTGAATGGGAAGATCA	964
QY	316	ArgLeuPheGluHisTyrSerAlaValAlaGlnArgIleGlyValTyrThrAlaAsnAsp	335	
Db	965	AATCTATTGTAACACTCTCTGCTGTGGCGGCAACGTTATGGAGTGAACACTGACAGAGAC	1024	
QY	336	TyrTrpAlaSerIleLeuGluPheLeuValGlnArgTrpArgLeuGluLysLeuGluGlyLeu	355	
Db	1025	TATCTGTATATATGGAAATATCTATGATGGCGGAGATGGAGGTGGAGAAAGCTGACAGGCTT	1084	
QY	356	MetaAlaGluLysIleArgAlaGlnAlaGlnAspPheValLysGlyLeuAlaProArgIleArgArg	375	
Db	1085	ACAGAGAGAGGCGCGTAAAGCCACAGAGATGTGTGTGCTTGCGCTCCAGAGATCAGAAGG	1144	
QY	376	LeuGlnGluArgAlaGlnAspGluArgAlaArgLysMetLysLysHisGlyValLysPhe	395	
Db	1145	TTGGATGAGAGACGACAGGACGTCGA-----AAGGACAGACGCGCTGCCCCCTT	1195	
QY	396	SerTrpIlePheAsnLysGluLeuLeuLeu 405		
Db	1196	ACATGATTTTGGCCGAGAAAGTGTGCTC 1225		
RESULT 11				
POSSACPD	1507 bp	mRNA	linear	PLN 27-APR-1993
LOCUS	Solanum tuberosum stearoYL-acyl carrier protein desaturase mRNA,			
DEFINITION	complete cds.			
ACCESSION	M91238			
VERSION	M91238.1 GI:169564			
KEYWORDS	stearyl-acyl carrier protein desaturase.			
SOURCE	Solanum tuberosum cDNA to mRNA.			
ORGANISM	Solanum tuberosum			
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.			
AUTHORS	1 (bases 1 to 1507)			
TITLE	Taylor,M.A., Smith,S.B., Davies,H.V. and Birch,L.R.			
JOURNAL	The primary structure of a cDNA clone of the stearyl-acyl carrier protein desaturase from potato (Solanum tuberosum L)			
FEATURES	Unpublished (1992)			
source	Location/Qualifiers			
	1..1507			
	/organism="Solanum tuberosum"			
	/db_xref="taxon:4113"			
	56..1237			
CDS	/codon_start=1			
	/product="stearyl-acyl carrier protein desaturase"			
	/protein_id="AA33839.1"			
	/db_xref="GI:169565"			
	/translation="MALNINQVSLKSHKMLPFCCSARSEVFMASTIHRPSVEVGSV			
	KKATPREVEHVQYTHSMPEKIEVDFSLRPMANONLIVHLKPYEKQWQDFLPDPDP			
	SEGDGEQVKELEKREKELPDYFVYLIGDMTELEALPYQTMNLDDVREGTAVYDPA			
	PMALITRAMTAENRKHGLINKLYISGRVMDKIETKIQVLIQSGMDPRENNPPYIG			
	FVYSLSKRGYTFVSHGNARAKLEGHMKLAQIGTSGIAADKRREHATYTKYVLELPE			
	DDPAVALIIGDMKRNTSMRPHMLITDGDNLFEHFSVAQRLGVYAKDVADLLEH			
	VGRNEVEKLTLGSSBGRADQYVGLAPRIKLERRAQRARAKKASVPSFWIKREIKM			
	L"			
	polyA_signal 1423..1428			
BASE COUNT	423 a 293 c 369 g 422 t			
ORIGIN				
Alignment Scores:				
Pred. No.:	9.13e-98	length:	1507	
Score:	1306.00	Matches:	250	
Percent Similarity:	75.57%	Mismatch:	50	
Best Local Similarity:	62.97%	Indels:	30	
Query Match:	60.74%	Gaps:	5	
DB:				
US-09-934-900-2 (1-405) x POSSACPD (1-1507)				
QY	27	SerIleThrTrpGlnThrLeuProGlnLeuProCysSerSerArgLysAlaHis-----	44	

[illegible]

QY 389 LysHISglYValIysPheSerTrpIlePheAsnIysGluLeuLeu 405  
 Db 1193 -----TCGTTCCCTTCAAGCTGATTTTGTAAAGAGATTAAAGCTG 1234

## RESULT 12

AY087294

LOCUS 1651 bp mRNA linear JUN 26-JUN-2002

DEFINITION Arabidopsis thaliana clone 33739 mRNA, complete sequence.

ACCESSION AY087294

VERSION AY087294.1 GI:21406018

KEYWORDS FLI\_CDNA.

SOURCE Chlae cress.

ORGANISM Arabidopsis thaliana

Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE 1 (bases 1 to 1651)

Haas,B.J., Volfovsky,N., Town,C.D., Troukhan,M., Alexandrov,N.,

AUTHORS Feldmann,K.A., Flavell,R.B., White,O. and Salzberg,S.L.

TITLE Full-length messenger RNA sequences greatly improve genome

JOURNAL annotation

REFERENCE Genome Biol. (2002) In press

AUTHORS 2 (bases 1 to 1651)

Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and

Feldmann,K.

TITLE Full-length cDNA from Arabidopsis thaliana

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 1651)

Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and

Feldmann,K.

TITLE Direct Submission

JOURNAL Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road,

COMMENT Malibu, CA 90265, USA

This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the C-terminal end of the encoded protein. Please note that these cDNA sequences are derived from the WS or Laer ecotypes and therefore may contain polymorphisms when compared to sequences from Col-0. Genet carried out the library production and sequencing of the full-length clones. Ceres, Inc. carried out the clustering of the 5' sequences, selection of clones, and sequence assembly.

## FEATURES

source

/organism="Arabidopsis thaliana"

/db\_xref="taxon:3702"

/clone="33739"

CDS 132..1322

/codon\_start=1

/product="putative stearyl-acyl carrier protein

desaturase"

/protein\_id="AA064846.1"

/db\_xref="GI:21592896"

/translation="MAMAMDRIVFSPSSVYLPCQAGSRSSRVSMASTIRATTEVT

NQRKLYIPREHVQVYKSMPOKLEIFSLGMADETLATLTKPEKSMQPTDEIPE

PSESEFYDQVKELEKREKELPDYFVYLVDGMDTEALPTOTMLTLDGVDENGAS

PTPMIAWTRAWTAENRBDGLNKLYLISGRVDMQIEKTIQYLLGSGNDPTENNPY

LGFITTSRERATFISHGNTALANDKGLKAQICGTIADBERRERATYRTIVKLE

ETDPGDTILGLADMKKTSMPAHLMVDQDNLFEHFTVAQRUGVYAKDYADILE

FLVERMNETLLDLSSEGRADFCVGLPARIRKIIEAQAQAKAKNIPSWIFGR

BASE COUNT

ORIGIN

Alignment Scores:

Pred. No.: 2,63e-97 Length: 1651  
 Score: 1301.00 Matches: 244  
 Percent Similarity: 77.89% Consistency: 52  
 Best Local Similarity: 64.21% Mismatches: 64  
 Query Match: 60.51% Indels: 20  
 DB: 8 Gaps: 5

US-09-934-900-2 (1-405) x AY087294 (1-1651)

QY 24 ThrGYSHisSerLlePheThrGlnPheProGlnLeuProCysSerArgLysAla 43

Db 234 ACGATTGCTGCTGCGACTACAGAGCTT-----ACGATGGAAGAACTG 278

QY 44 HISHSARGHISLeuLeuProPheAsnAlaAlaValSerAlaAlaProPheLysAla 63

Db 279 TAT-----ATCCCTCCACAGAGGTCAGTCCAAAGTC----- 311

QY 64 ArgLysAlaHISerMetProGluLysGluIlePheLysSerLeuLugLyr 83

Db 312 -----AAACATTCATAGCCGCCACAAAGTTAGACATCTTAAAGCTTAAAGGATCG 365

QY 84 AlaserGluTrpValLeuProLeuLysProValGluGlnCysTrpGlnProGlnAsn 103

Db 366 GCTGATGAAACCTGCTGCTGCTTATTTAAACCTGTTGAGAAATCGTGCACCTACCGAT 425

QY 104 PheLeuProAspProSerLeuProHISgluIlePheSerHISgluValLysGluLeuArg 123

Db 426 TTCTTCCCGAAGCTGAG-----TCGGAAGATTCGTATGACCAAGTCAAGAGCTTAAG 479

QY 124 GluArgThrLysGluLeuProAspGluLyrPheValValLeuValGluLysPheValThr 143

Db 480 GAAGGTGCAAGCAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 539

QY 144 GluAspAlaLeuProThrLysGlnPheMetIleAsnAsnLeuAspGluValLysAspAsp 163

Db 540 GAAGAACCTTCT 599

QY 164 SerGlyThrSerProSerProThrAlaValIleThrArgAlaIleThrAlaGluGluAsn 183

Db 600 ACAGGAGCTAGTCT 659

QY 184 ArgHISglYAspLeuLeuArgThrLysGluLysSerGlyArgValAspMetLysAlaLys 203

Db 660 AGACATGGGAGATCTCTTAACAGATATCTTATCTGTGTGGGTGATACATGAGCGAG 719

QY 204 ValGluLysThrValHISLysLeuIleSerAlaGluMetAspProGlyThrAspAsnAsn 223

Db 720 ATTGAAACATCTATCTAGTACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 779

QY 224 ProTyrLeuGlyPheValIleThrSerPheGlnGluArgAlaIleThrPheValAlaHISglY 243

Db 780 CCTTACTTGGTTCATCTACACATCATCTTCAAGAAAGCGACCTTCCTCCCTGGA 839

QY 244 AsnThrAlaArgLeuAlaLysGluLysGlyAspProValLeuAlaArgLeuGlyThr 263

Db 840 AACACTGCCAGACTGCGAAGATCTGCGAGATTTGAACCTTGGCGAGATATGAGGAGAC 899

QY 264 IleAlaAlaAspGluLysArgHISgluAsnAlaLysSerArgIleValGluLysLeuLeu 283

Db 900 ATTGCGCTGATGAGAGGCGCTCATGAGACTGCTTACACCAAGTTGTATAGAAAGCTCTT 959

QY 284 GluValAspProThrGlyAlaMetValAlaIleGlyAsnMetMetGluLysLysIleThr 303

Db 960 GAAATGACCTGATGAGAGGCGCTGCGCTGCGCTGATATATGAAAGAAAGATATCA 1019

QY 304 MetProAlaHISLeuMetLysArgLysGluLysAspProArgLeuPheGluLysIleSerAla 323

Db 1020 ATGCGCTGACATTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1079

QY 324 ValAlaGlnArgIleGlyValIleThrAlaAsnAspTyrAlaAspIleLeuGluPheLeu 343

Db 1080 GTTGCCAGAGGCTGCTGTCTACACTGCGCAAGAGCATGCTGATATTTCTGAGATTCTT 1139

QY 344 ValGluArgTPArgLeuGluLeuGluMetAlaGluGlyLysArgAlaGln 363  
 Db 1140 GTTGAACGGTGGAAATGTGAGACTTTGACAGACCTTTAGTAGAGGACAGCCGAC 1199  
 QY 364 AspPheValLysGlyLeuAlaProArgLysArgLeuGluGlnAlaAspLysArg 383  
 Db 1200 GACTTGTCTGGGACTCTGACAGAAATCCGTAATAATGAAGAGAGCTCAAGAGA 1259  
 QY 384 AlaArgLysMetLysLysHisHisGlyLysPheSerTrpLysPheAsnLysGluLeu 403  
 Db 1260 GCCAAGAGAGCTGCCAAGAAC-----ATACCATTCAGCTGGATATTTGGTGAATATTC 1313  
 RESULT 13  
 LOCUS 113990 2243 bp DNA linear PAT 26-SEP-1995  
 DEFINITION Sequence 1 from patent US 5443974.  
 ACCESSION 113990  
 VERSION 113990.1 GI:996440  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 2243)  
 AUTHORS Hitz,W.D., Yadav,N.S. and Perez-Grau,L.  
 TITLE Nucleotide sequence of soybean stearyl-ACP desaturase gene  
 JOURNAL Patent: US 5443974-A 1 22-AUG-1995;  
 FEATURES  
 source location/Qualifiers  
 1..2243  
 BASE COUNT 625 a 447 c 528 g 643 t  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 4.69e-97 Length: 2243  
 Score: 1300.00 Matches: 250  
 Percent Similarity: 74.82% Conservative: 56  
 Best Local Similarity: 61.12% Mismatches: 73  
 Query Match: 60.47% Indels: 30  
 DB: 6 Gaps: 6  
 US-09-934-900-2 (1-405) x 113990 (1-2243)  
 QY 15 HisValIleLysThrMetGlnIleArgThyCysHisSerIleThrGlnThr----- 32  
 Db 52 CATGACTACTACTATCAATGAGCTGTGAGACTGAACCTATCCACCAACCTTCTCC 111  
 QY 33 LeuProGlnLeuPro-----Cys 38  
 Db 112 CTCCCAAGATGCCCCAGCTCCCGCTTCCGCATGGCTTCCACCTCCGCTCC 171  
 QY 39 SerSerArgLysAlaHisHis-----ArgHisLeuLeuProProLeuAsnAlaAlaVal 56  
 Db 172 GGTTCAGAGAGGTTGAATAATTAAGAGCCATTCACTCCCTCCAGAGAACTGATGTT 231  
 QY 57 SerAlaAlaProPheLysAlaLysAlaHisSerMetProProGluLysLysGluLeu 76  
 Db 232 CAAGAA-----ACCCACTATGCCCTCCCAAGAGATTGAGATT 270  
 QY 77 PheLysSerLeuGluGlyTrpAlaSerGluTrpValLeuProLeuLeuLysProValGlu 96  
 Db 271 TTCAATCTTTGGAGATGTGGCTGACCAAGAACATCTGACTCATCTTAACCTGTAGAA 330  
 QY 97 GlnCysTrpGlnProGlnAsnProLysPheProSerLeuProHisGlnLysLeuSer 116  
 Db 331 AAATGTGGCAACACAGAGATTTTACCCGACCCCTCC-----TCAGATGGAATTGAA 384  
 QY 117 HisGlnValLysGluLeuArgLysArgLysGluLeuProAspGluTrpPheValVal 136  
 Db 385 GAGCAAGTGAAGAACTGAGAGAGAGCAAGAGATTCAGAGATTAATTCTTGTGTT 444  
 QY 137 LeuValGlyAspMetValThrGluAspAlaLeuProThrTrpGlnThrMetLeuAsn 156  
 Db 445 CTTTGGAGAGCATGATACAGAGAGAGCTGTGCTACTTACCAAACTATGTTAAATACT 504

QY 157 LeuAspGlyValLysAspAspSerGlyThrSerProSerProTrpAlaValTrpThrArg 176  
 Db 505 TTGGATGGAGTTCGTGATGAAACAGAGCTGCCAGCTTACTCTGGGCAATTTGGACAAAG 564  
 QY 177 AlaTrpTrpAlaGluGlnAsnArgHisGlyAspLeuLeuArgThrTyrrLeuTrpLeuSer 196  
 Db 565 GCATGAGACTGTGAAGAAACAGACAGCGTATCTTCAACAAATATCTGTACTGAGT 624  
 QY 197 GlyArgValAspMetAlaLysValGluLysThrValHisTyrrLeuIleSerAlaGluMet 216  
 Db 625 GGACAGAGTGGACATAAACAAATTGAGAGAACAAATTCAGTACTTATGGGCTGGAGT 684  
 QY 217 AspProGlyLysAspAsnAsnProTrpLeuGlyPheValTyrrThrSerPheGlnLysArg 236  
 Db 685 GATCTCGGACCGAAGACAGCCCTTACTGTGTTCAATTATTCATCTTCAATTAAGAGAG 744  
 QY 237 AlaTrpPheValAlaHisGlyAsnThrAlaArgLeuAlaLysGluGlyLysAspProVal 256  
 Db 745 GCACCTTCATATCCACGGAACACAGCGCAGCTTGGCAAGAGACATGTCATATAA 804  
 QY 257 LeuAlaArgLeuCysGlyThrThrAlaAlaAspGluLysArgHisGlnAsnAlaTrpSer 276  
 Db 805 TTGGCAGAGATCTGGCGCATGATGCTCAGATGAGAAAGCCAGAGACTCATATACACA 864  
 QY 277 ArgIleValGlnLysLeuLeuGlnValAspProThrGlyAlaMetValAlaIleGlyAsn 296  
 Db 865 AAGATATGGAAGAACTGTTGAGGTGATGCTGATGAGTATGAGCATTTGCCGAC 924  
 QY 297 MetMetGluLysLysIleThrMetProAlaHisLeuMetTyrrAspGlyAspAspProArg 316  
 Db 925 ATGATGAGAGAAAGAAATGCTGATGCCAGACACCTTATGATAGAGCGCGCAGCAAC 984  
 QY 317 LeuPheGlnHisTyrrSerAlaValAlaGlnArgIleGlyValTyrrThrAlaAsnAspTrp 336  
 Db 985 CTGTTGATTAACACTACTGCTCCGCTCCGCGAGCCATGGGGCTACACTGCAAGAGACTAT 1044  
 QY 337 AlaAspIleLeuGlnPheLeuValGluArgTrpArgLeuGlnLysLeuGluLysMet 356  
 Db 1045 GCTGACATATCTGAATTTCTGGTGGAGAGTGGAAGTGGACAGCTGACCCGACTTCA 1104  
 QY 357 AlaGluGlyLysArgAlaGlnAspPheValCysGlyLeuAlaProArgLysArgLeu 376  
 Db 1105 GGTGAGGAGAGAAAGCTGAGAAATAGCTTTTGGGCTCCCAAGATCAAGAAAGTTG 1164  
 QY 377 GlnGluArgAlaAspGluArgLysAlaArgLysMetLysLysHisGlyValLysPheSer 396  
 Db 1165 GAGGAGAGAGCTCAAGCAAGAGGC-----AAGGAGTCTCAACACTTAATTCAGT 1215  
 QY 397 TrpIlePheAsnLysGluLeuLeuLeu 405  
 Db 1216 TGGATTCATGACAGGAGAGTACTACTC 1242  
 RESULT 14  
 LOCUS 1643 bp mRNA linear PLN 22-AUG-1995  
 DEFINITION Ricinus communis stearyl-acyl-carrier protein desaturase mRNA, 3' end of cds.  
 ACCESSION M59857  
 VERSION M59857  
 KEYWORDS fatty acid synthetase; lipid metabolism; stearyl-acyl-carrier protein desaturase.  
 SOURCE Ricinus communis developing seed cDNA to mRNA.  
 ORGANISM Ricinus communis  
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Malpighiales; Euphorbiaceae; Ricinus.  
 REFERENCE 1 (bases 1 to 1643)  
 AUTHORS Shanklin,J. and Somerville,C.  
 TITLE Stearyl-acyl-carrier-protein desaturase from higher plants is structurally unrelated to the animal and fungal homologs  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 88 (6), 2510-2514 (1991)  
 MEDLINE 91172837



Search completed: May 30, 2003, 06:14:23  
Job time : 3448 secs

**THIS PAGE BLANK (USPTO)**